Fig. 1

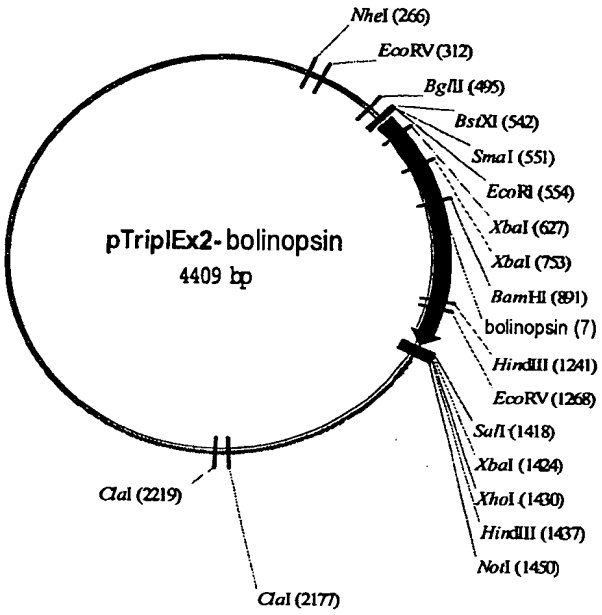
NheI (266)
EcoRV (312)
BglII (495)
BstXI (542)
SmaI (551)
EcoRI (554)
XbaI (627)
XbaI (753)
BamHI (891)
bolinopsin (7)
HindIII (1241)
EcoRV (1268)
SalI (1418)
XbaI (1424)
XhoI (1430)
HindIII (1437)
NotI (1450)
ClaI (2177)
ClaI (2219)
pTriplEx2-bolinopsin
4409 bp

Fig. 2

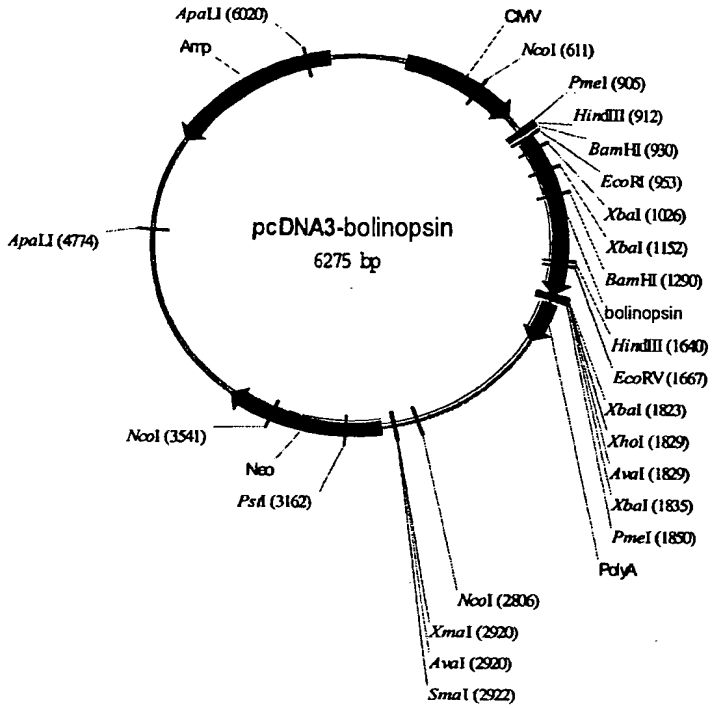
pcDNA3-bolinopsin
6275 bp
ApaLI (6020)
Amp
CMV
NcoI (611)
PmeI (905)
HindIII (912)
BamHI (930)
EcoRI (953)
XbaI (1026)
XbaI (1152)
BamHI (1290)
bolinopsin
HindIII (1640)
EcoRV (1667)
XbaI (1823)
XhoI (1829)
AvaI (1829)
XbaI (1835)
PmeI (1850)
PolyA
NcoI (2806)
XmaI (2920)
AvaI (2920)
SmaI (2922)
NcoI (3541)
Neo
PstI (3162)
ApaLI (4774)

Fig. 3

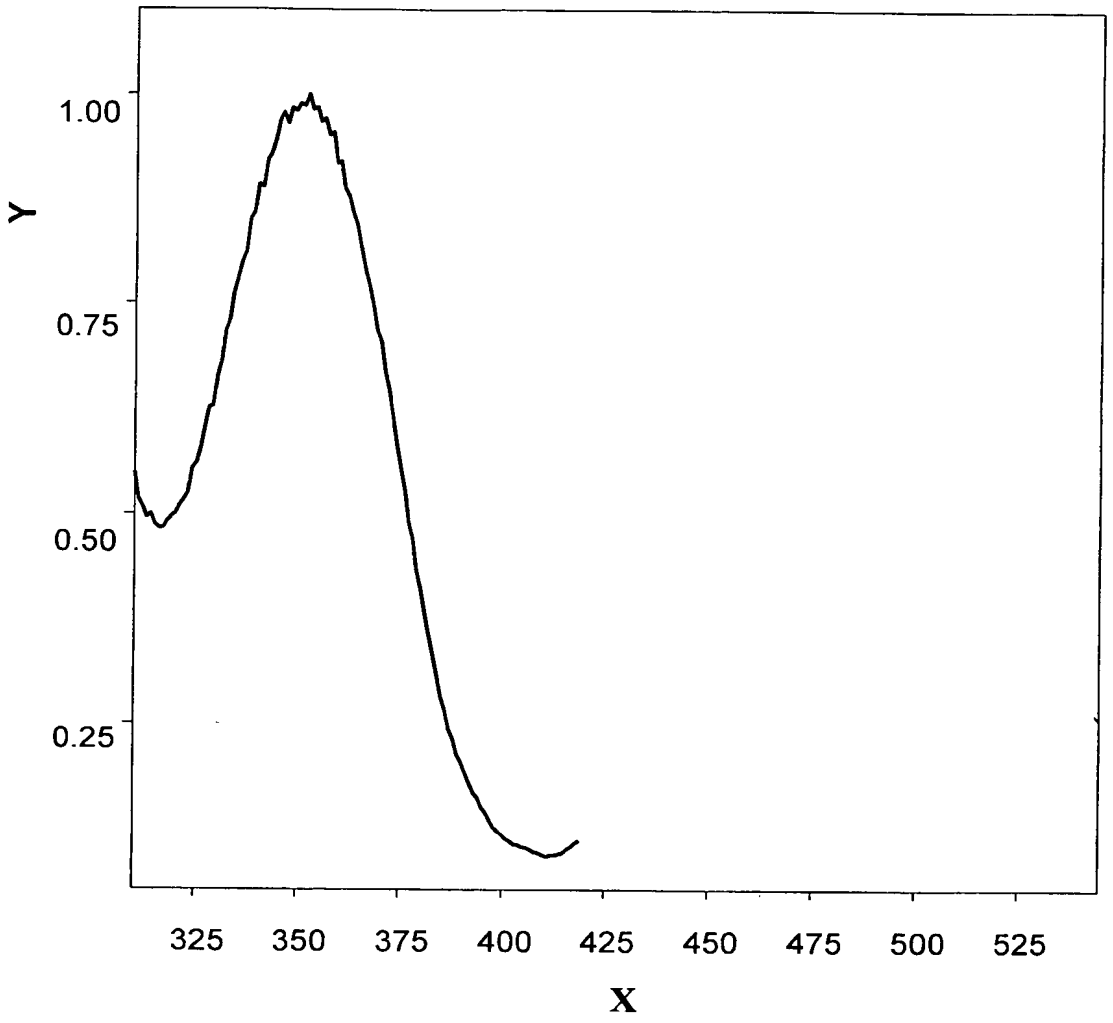

Fig. 4

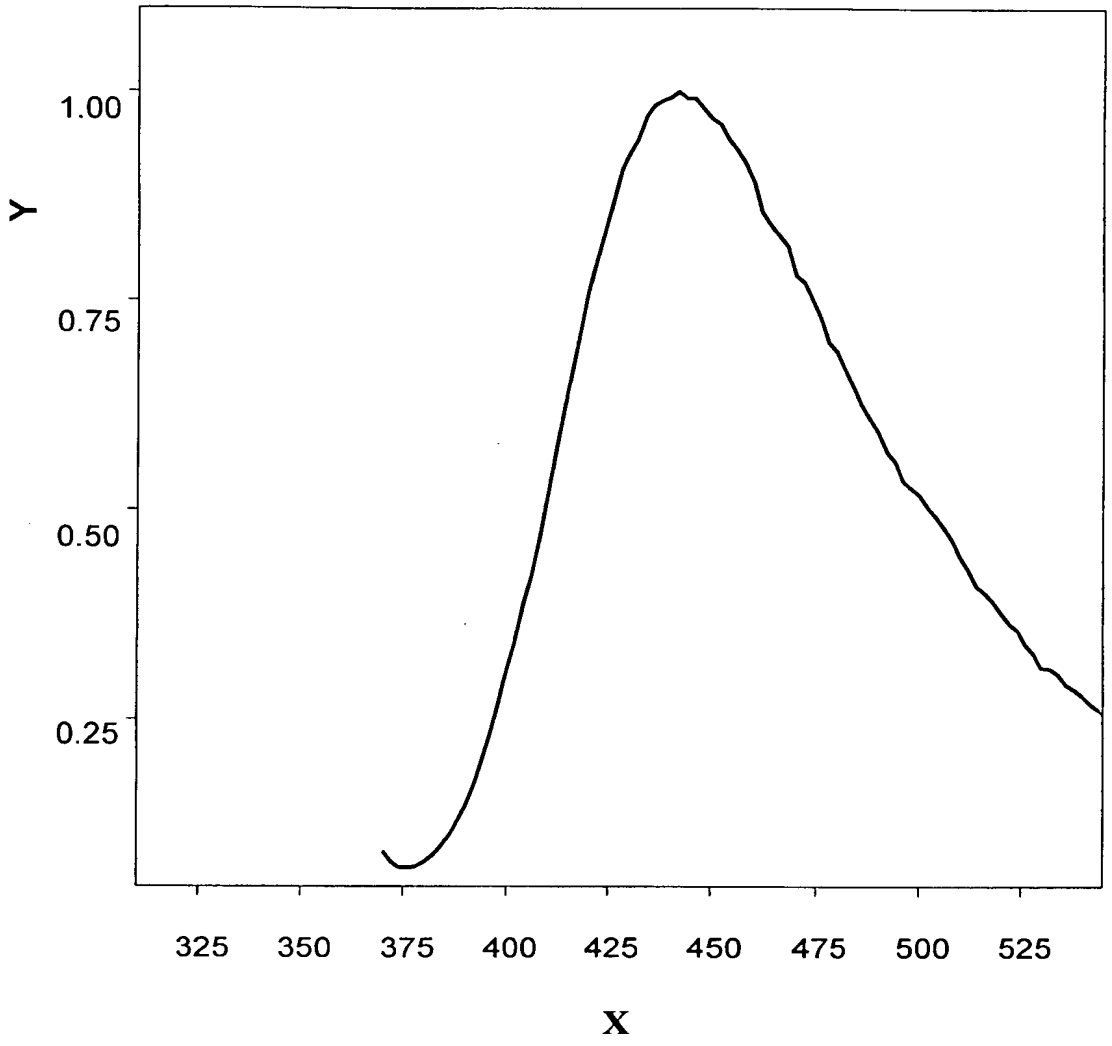

Fig. 5

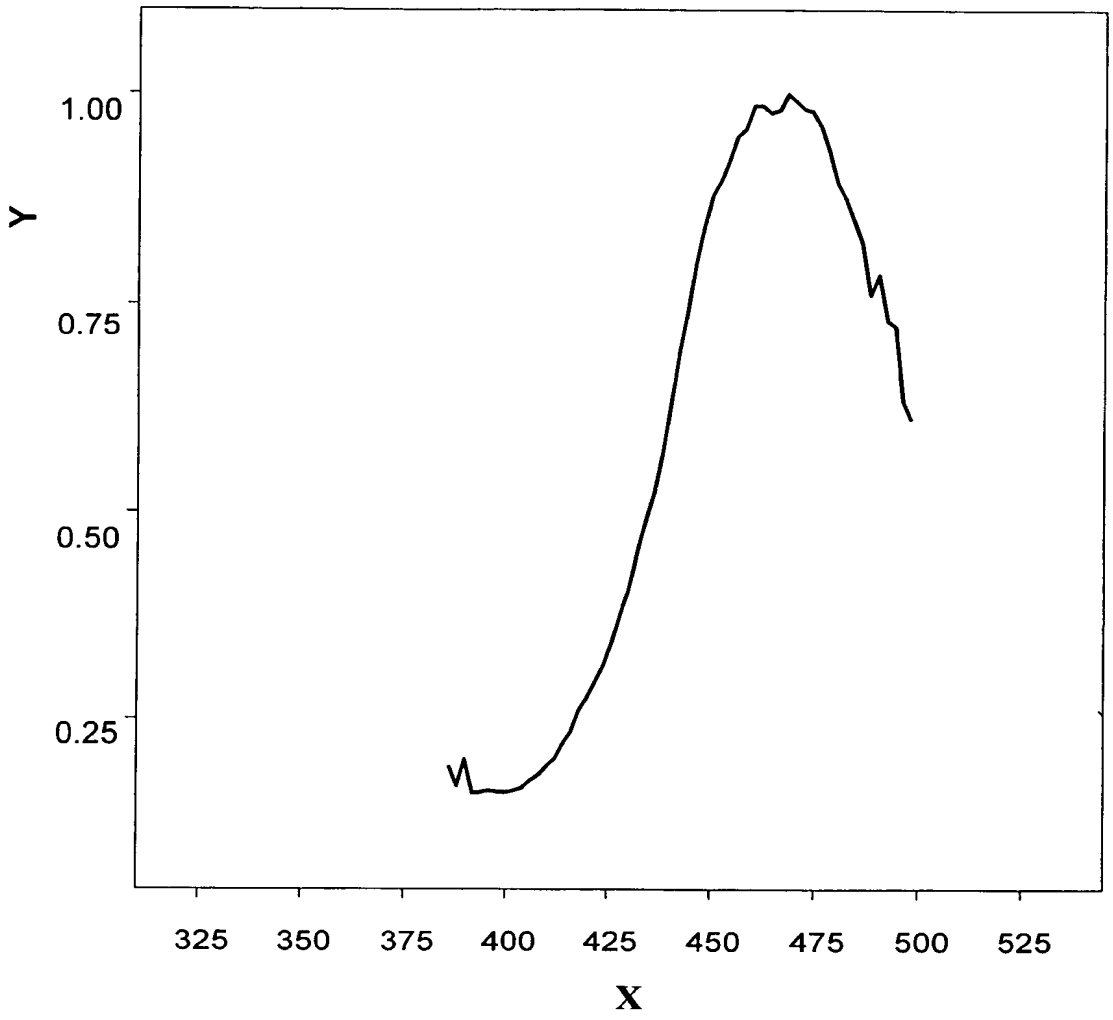

Fig. 6

```
aequorin   _000:ATGACAAGCAAACAATACTCAGTCAAGCTTACATCAGACTTCGACAACCCAAG--ATGGA
score      _000:ATG         C    CTC         TA A  AGAC  C ACAAC  AAG  AT GA
bolinopsin_000:ATG---------C----CTC---------TAGACGAGAC--CAACAACGAAAGCTATAGA

aequorin   _060:TTGGACGACACAAGCATATGT-TCAATTTCC---TTGATGTCAACCAC---AAT-GGAAA
score      _060: TGG  G  A AAG  T  GT  C ATT  C   TTGATGTC A  AC    AT   AAA
bolinopsin_060:-TGGCTG--AGAAGTGTGGGTAACGATTGGCAGTTTGATGTCGAGGACGTTCATCCTAAA

aequorin   _120:AATCT-------CTCTTGACGAGATGGTCTACA-AGGC-ATCT-GATATTGTC-ATC-AA
score      _120: A CT       CTCT  A GAGAT  TC ACA    C ATCT GA A TG C  TC  A
bolinopsin_120:CAGCTTAGTCGGCTCTACAAGAGAT--TCGACACCTTCGATCTAGACAGTGACGGTCGTA
```

Fig. 6 continued

```
aequorin  _180:TAACCTTGGAGCAACA-CCTGAGCAAGCCAAACGACACAAAGA---TGCTGTAGAAGCCT
score     _180:T   C TGGA C A A CCTG  C  GCC   CGACA AA GA    GCTG  GAA  CT
bolinopsin_180:TGGACATGGA-CGAGATCCTGTACTGGCC---CGACAGAATGAGGCAGCTGGTGAACGCT

aequorin  _240:TCTTCGGAGGAGCTGGAATGAAATATGGTGTGGAAACTGATTG----GCCTGCAT--ATA
score     _240:TCT   GA  AG T GA  GAA    G TG GG   CTG TTG     CCT C T  A A
bolinopsin_240:TCTGACGAACAGGTCGA--GAA----GATGAGG--GCTGCTTGCTACACCTTCTTCCACA

aequorin  _300:TTGAAGGA-TGGA---A-AAAATTGGCTACT----GATGAAT---TGGAG---AA-----
score     _300:   AAGGA TGGA   A AAAA  G CT CT    GA GA T   T GAG   AA
bolinopsin_300:ACAAAGGAGTGGATCCAGAAAAGGGACTCCTCAGAGACGACTGGGTTGAGGCTAACAGAG
```

Fig. 6 continued

```
aequorin  _360:-AT------ACGCCAAAA-----ACGAACCAACG---------CTC----ATCCGTATAT
score     _360: AT      A GC  AAA     A G A C ACG         CTC    AT  GT T T
bolinopsin_360:TATTTGCTGAGGCTGAAAGAGAGAGGGAACGACGTGGCATGCCCTCCTTGATTGGTCTTT

aequorin  _420:GGGGTGATGCTTTGTTTGATATCGTTGACAAAGATCAAAATGGAGCCATTACACTGGATG
score     _420: G   GA GCTT  T  GAT TC T GA  A GA     ATGG  C  TT    T GATG
bolinopsin_420:TGTCAGACGCTTACTACGATGTCCTGGATGATGACGGTGATGGTACTGTTGATGTTGATG

aequorin  _480:AA-TGGAAAGCATACACCAAAGCTGCTGGTATCATCCAATCATCAGAAGATTGGGAGGAA
score     _480:AA T  AAA CAT  A  AA GCT  TG  AT   CC   C  CAG AG  T  G   A
bolinopsin_480:AACTCAAAACCAT-GATGAAGGCTTTTG--ATGTGCC---C--CAGGAGGCT--GCCTAC
```

Fig. 6 continued

```
aequorin  _540:ACATTC---AGAGTGTGC-GATATTGATGAAAGTGGACAACTCGATGTTGATGAGATGAC
score     _540:AC TTC   A AG   GC GA A  GAT A AGTGGA AACT GA G  GA G GA  AC
bolinopsin_540:ACCTTCTTTA-AGAAAGCTGACACGGATAATAGTGGAAAACTGGA-G-AGAAGCGA--AC

aequorin  _600:AAGACAACAT---TT-AGGA--TTTTGG-T--ACACCATGGATCCTGCTTGCGAAAAGCT
score     _600:  G C  CAT   TT AG A  TT TGG T  A  CC   GATCCT   TG GA     T
bolinopsin_600:TGGTC--CATCTCTTCAGAAAGTTCTGGATGGAATCCTACGATCCTCAGTGGGACGGTGT

aequorin  _660:CTACG-GTGGAGCTGTCCCCTAA
score     _660:CTACG  T  A  T T    TAA
bolinopsin_660:CTACGCTTACAAATAT----TAA
```

Fig. 7

```
AEQUORIN  _000:VKLTP-DFDNPKW---IG---------RH-KHM------FNFLDVNHNGRISLDEMVYKA
score     _000:  L |  ||  |W   |G          H K||      F  |D| | GR| |DE||Y|
BOLINOPSIN_000:MPLDETNNESYRWLRSVGNDWQFDVEDVHPKQLSRLYKRFDTFDLDSDGRMDMDEILYWP

AEQUORIN  _060:SDIVINNLGATPEQAKRHKDAVEAFFGGAAMKYGVETEWPEYIEGW----KRLASEELKR
score     _060: D   | | A |EQ||||||A|  FF    |  GV| E|  | | W    | |A  E |R
BOLINOPSIN_060:-DRMRQLVNASDEQVEKMRAACYTFF----HNKGVDPEKGLLRDDWVEANRVFAEAERER

AEQUORIN  _120:YSKNQITLIRLWGDALFDIIDKDQNGAISLDEWKAYTKSAGIIQSSEDCEETFRVCDIDE
score     _120:  |    LI L  DA||D| D D  G | |DE K | K|  | Q  E|    F|  D|D
BOLINOPSIN_120:ERRGMPSLIGLLSDAYYDVLDDDGDGTVDVDELKTMMKAFDVPQ--EAAYTFFKKADTDN
```

Fig. 7 continued

```
AEQUORIN   _180:SGQLDVDEMTRQHLG--FWY-TMDPACEKLYGGAV---P
score      _180:SG|L|  E|   HL   FW|  |DP     | G||
BOLINOPSIN_180:SGKLERSEL--VHLFRKFWMESYDP----QWDGVYAYKY
```

Fig. 8

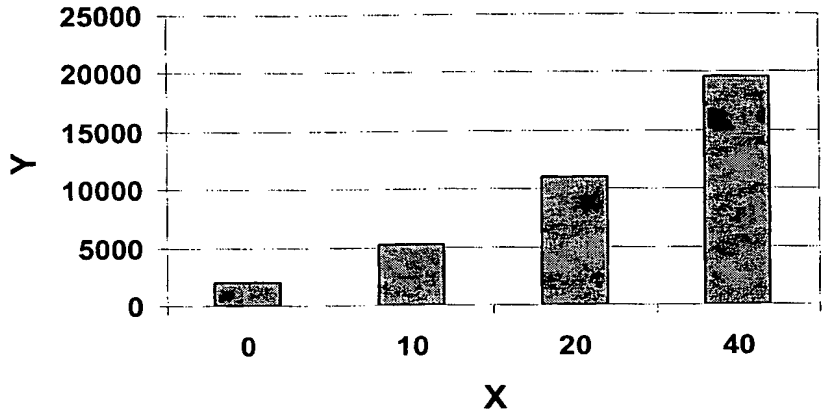

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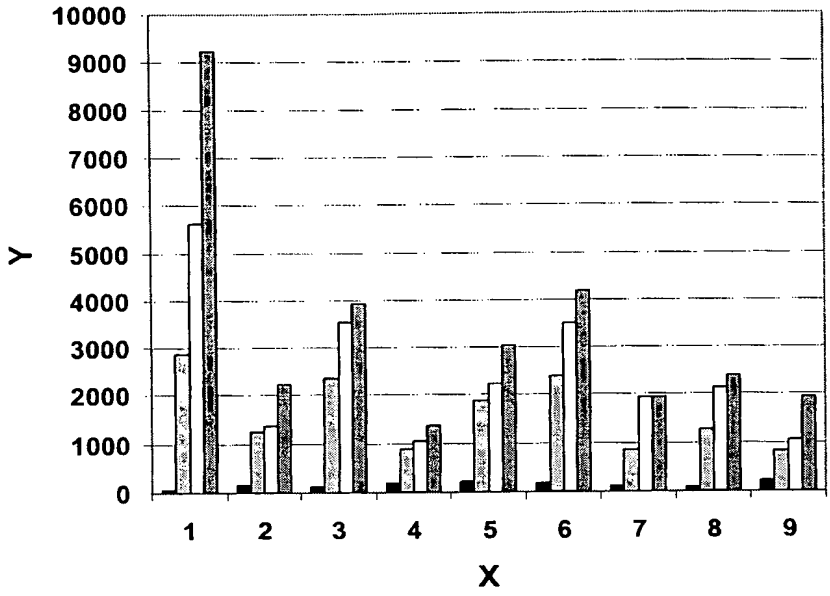
Fig. 9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